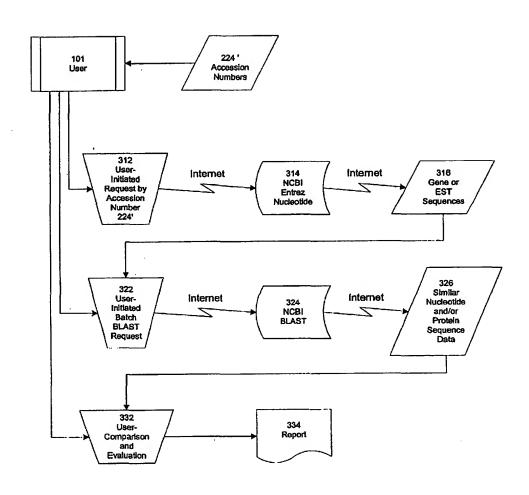
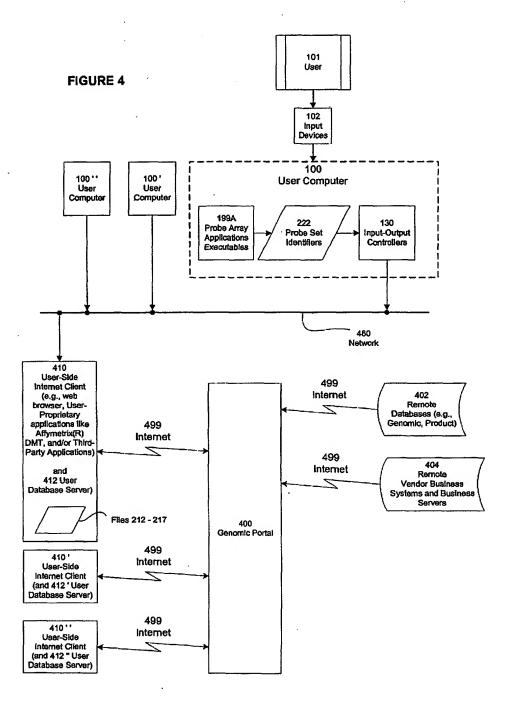


FIGURE 3 (PRIOR ART)





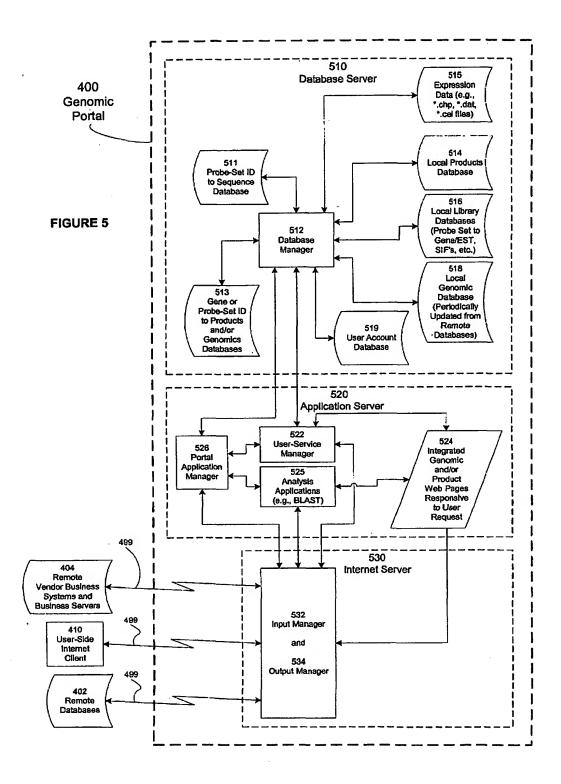
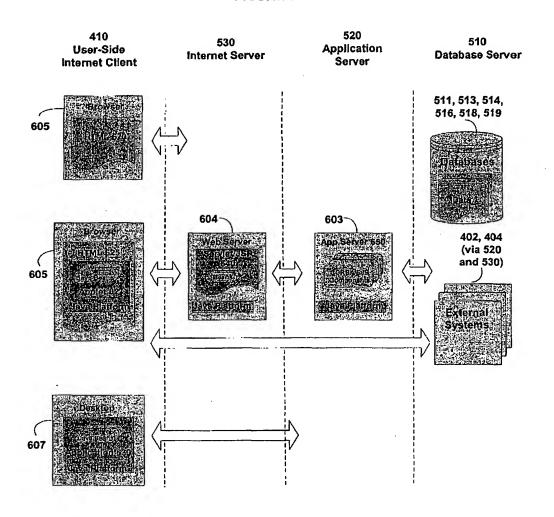
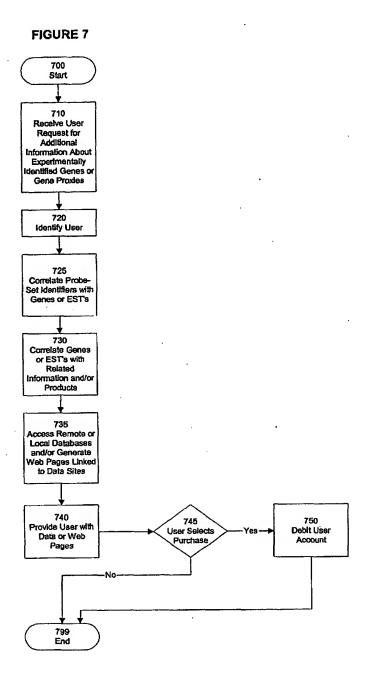
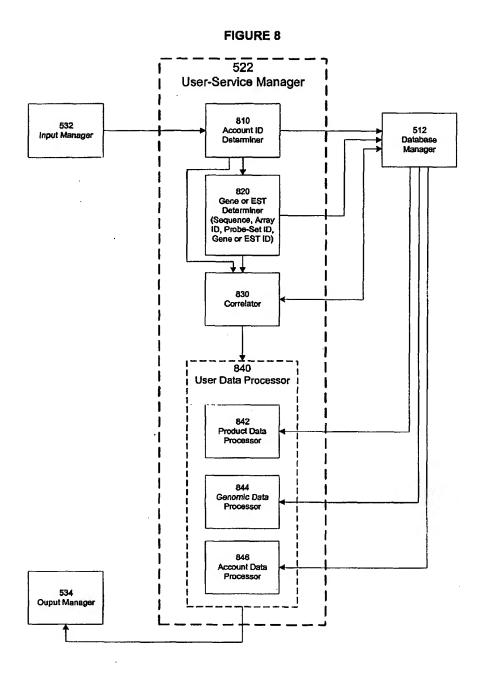
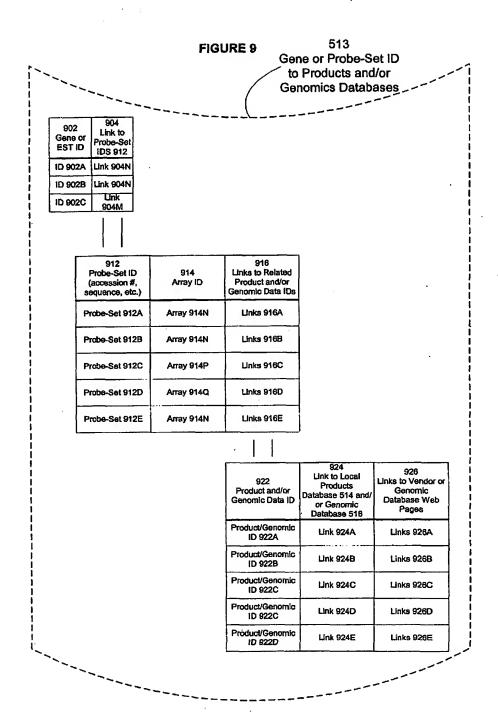


FIGURE 6









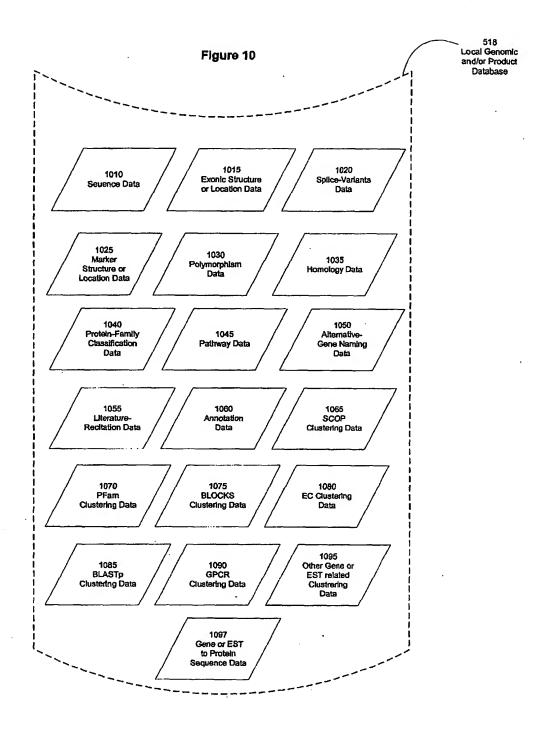
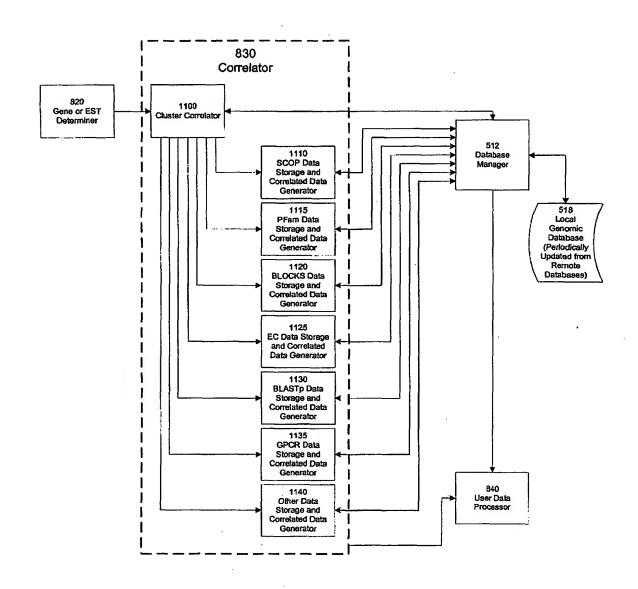


Figure 11



## Figure 12

```
1200
                    GUI
                                                      1210
                                                   Cluster Method
Identifier
   1240
                                                                    1220
Protein Identifier
                                                                Returned Family
             Domains PFAM Hs:NP 003828
                                                                    Data
                               NP_003828
             SEARCH METHOD
                                hmmpfam-
             HIT NAME
HIT DESC
                                FBPase WUSTL
                                Fructose-1-6-bisphosphatase
                                1.5e-179 LOG10 -179
Query 12 _ 335 Target 1 _ 342; EXPECT 1.5e-179 LOG10 -
             OVERALL_EXPECT
             SIMSPAN
             179;
             ALIGNMENT
             FBPase: domain 1 of 1, from 12 to 335: score 609.9, E = 1.5e-179
                                   *->iTLtrfileeqgedalaKNEatgeltdlLssLalaakeiartIarag
                                       +TLtr ++e+ g+ a+
                                                              tgelt+lL+s +a k+i+++++ag
                                       LTLTRYVMEK-GRQAK----GTGELTQLLNSMLTAIKAISSAVRKAG
                 NP_003828
                                   {\tt LanllGlagatNsqGDeQKkLDViaddifinALkasgvvavlaSERedel}
                                   La+l+G+ag++N++GDe+KkLDV+++ ++in+L++s ++vl+SEE++++
                 NP_003828
                                54 LAHLYGIAGSVNVTGDEVKKLDVLSNSLVINMLQSSYSTCVLVSEENKDA
              103
                                                                                        1230 /
Returned Alignment
              //
```